

SCORE Search Results Details for Application 10803459 and Search Result us-10-803-459c-8.rag.

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OM protein - protein search, using sw model

```
Run on:      September 27, 2006, 13:36:31 ; Search time 199 Seconds
              (without alignments)
              480.192 Million cell updates/sec
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Title: US-10-803-459C-8
Perfect score: 1124
Sequence: 1 MAVDVNINIKCETDGYLTKM.....LDGLGYWSNWSRSAYAAVKD 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1124	100.0	209	9	AED11792	Aed11792 Chicken 1
2	1124	100.0	209	9	AED40484	Aed40484 Chicken 1
3	1082.5	96.3	1146	4	AAE00961	Aae00961 Chicken 1
4	713.5	63.5	210	9	AED11786	Aed11786 Human lep
5	713.5	63.5	210	9	AED40478	Aed40478 Human lep
6	712.5	63.4	892	2	AAW34260	Aaw34260 Rat ob re
7	712.5	63.4	894	2	AAW37338	Aaw37338 Ob protei
8	712.5	63.4	894	2	AAW37337	Aaw37337 Ob protei
9	712.5	63.4	895	2	AAW34258	Aaw34258 Rat ob re
10	712.5	63.4	1015	2	AAW34259	Aaw34259 Rat ob re
11	712.5	63.4	1162	2	AAW23399	Aaw23399 Rat ob re
12	712.5	63.4	1162	2	AAW23398	Aaw23398 Rat ob re
13	712.5	63.4	1162	2	AAW34257	Aaw34257 Rat wild-
14	709.5	63.1	805	2	AAW22106	Aaw22106 Murine le
15	709.5	63.1	842	2	AAW22102	Aaw22102 Murine le
16	709.5	63.1	894	2	AAW24064	Aaw24064 Murine WS
17	709.5	63.1	894	2	AAW19114	Aaw19114 Murine sh
18	709.5	63.1	894	4	AAE12608	Aae12608 Murine sh
19	709.5	63.1	894	5	AAE25454	Aae25454 Murine Ob
20	709.5	63.1	894	5	AAE25764	Aae25764 Mouse sho
21	709.5	63.1	894	5	AAE23858	Aae23858 Murine Ob
22	709.5	63.1	894	7	ADC08952	Adc08952 Murine WS
23	709.5	63.1	894	8	ADG62977	Adg62977 Murine Ob
24	709.5	63.1	894	9	ADW88160	Adw88160 Murine WS
25	709.5	63.1	894	10	AEE75686	Aee75686 Murine Ob
26	709.5	63.1	894	10	AEF92870	Aef92870 Murine ob
27	709.5	63.1	900	2	AAW22105	Aaw22105 Murine le
28	709.5	63.1	1162	2	AAW19115	Aaw19115 Murine lo
29	709.5	63.1	1162	2	AAV13473	Aay13473 Peptide S
30	709.5	63.1	1162	4	AAE12615	Aae12615 Murine lo
31	709.5	63.1	1162	5	AAE25460	Aae25460 Murine Ob
32	709.5	63.1	1162	5	AAE25770	Aae25770 Mouse lon
33	709.5	63.1	1162	5	AAE23865	Aae23865 Murine Ob
34	709.5	63.1	1162	6	ABP72719	Abp72719 Mouse lep
35	709.5	63.1	1162	8	ADG63018	Adg63018 Murine Ob
36	709.5	63.1	1162	10	AEE75727	Aee75727 Murine Ob
37	709.5	63.1	1162	10	AEF92911	Aef92911 Murine ob
38	709.5	63.1	1162	10	AEF92924	Aef92924 Murine ob
39	709.5	63.1	1162	10	AEF92923	Aef92923 Murine ob
40	704.5	62.7	213	4	AAG63999	Aag63999 Amino aci
41	704.5	62.7	804	2	AAW34501	Aaw34501 Obesity r
42	704.5	62.7	804	7	ADB12853	Adb12853 Human lep
43	704.5	62.7	815	2	AAV05701	Aay05701 Human OB
44	704.5	62.7	839	2	AAW34502	Aaw34502 Obesity r
45	704.5	62.7	883	2	AAW62543	Aaw62543 Human ob-

ALIGNMENTS

RESULT 1

AED11792

ID AED11792 standard; protein; 209 AA.

XX

AC AED11792;

XX

DT 01-DEC-2005 (first entry)

SCORE Search Results Details for Application 10803459 and Search Result us-10-803-459c-8.r

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OM protein - protein search, using sw model

Run on: September 27, 2006, 13:45:26 ; Search time 52 Seconds
(without alignments)
351.806 Million cell updates/sec

Title: US-10-803-459C-8
Perfect score: 1124
Sequence: 1 MAVDVNINIKCETDGYLTKM.....LDGLGYWSNWSRSAYAAVKD 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	712.5	63.4	1162	2 US-08-803-346-1	Sequence 1, Appli

2	709.5	63.1	894	1	US-08-599-455B-2	Sequence 2, Appli
3	709.5	63.1	894	2	US-09-069-781B-2	Sequence 2, Appli
4	709.5	63.1	894	2	US-08-618-957A-12	Sequence 12, Appl
5	709.5	63.1	894	2	US-09-137-132-2	Sequence 2, Appli
6	709.5	63.1	894	2	US-08-864-564A-2	Sequence 2, Appli
7	709.5	63.1	894	2	US-09-094-410-2	Sequence 2, Appli
8	709.5	63.1	894	2	US-08-708-123D-2	Sequence 2, Appli
9	709.5	63.1	894	2	US-08-583-153A-2	Sequence 2, Appli
10	709.5	63.1	894	2	US-08-570-142D-2	Sequence 2, Appli
11	709.5	63.1	894	2	US-08-638-524B-2	Sequence 2, Appli
12	709.5	63.1	894	2	US-10-095-929-12	Sequence 12, Appl
13	709.5	63.1	894	2	US-09-950-149-2	Sequence 2, Appli
14	709.5	63.1	895	2	US-08-827-962-19	Sequence 19, Appl
15	709.5	63.1	895	2	US-08-827-962-21	Sequence 21, Appl
16	709.5	63.1	1162	1	US-08-599-455B-43	Sequence 43, Appl
17	709.5	63.1	1162	2	US-08-827-962-15	Sequence 15, Appl
18	709.5	63.1	1162	2	US-08-827-962-20	Sequence 20, Appl
19	709.5	63.1	1162	2	US-09-069-781B-43	Sequence 43, Appl
20	709.5	63.1	1162	2	US-09-137-132-43	Sequence 43, Appl
21	709.5	63.1	1162	2	US-08-864-564A-43	Sequence 43, Appl
22	709.5	63.1	1162	2	US-09-094-410-43	Sequence 43, Appl
23	709.5	63.1	1162	2	US-08-708-123D-43	Sequence 43, Appl
24	709.5	63.1	1162	2	US-08-638-524B-43	Sequence 43, Appl
25	709.5	63.1	1162	2	US-09-950-149-43	Sequence 43, Appl
26	704.5	62.7	569	1	US-08-306-231-3	Sequence 3, Appli
27	704.5	62.7	804	2	US-09-116-676-10	Sequence 10, Appl
28	704.5	62.7	883	2	US-08-982-430-1	Sequence 1, Appli
29	704.5	62.7	896	2	US-08-618-957A-10	Sequence 10, Appl
30	704.5	62.7	896	2	US-09-357-914-33	Sequence 33, Appl
31	704.5	62.7	896	2	US-08-780-562-3	Sequence 3, Appli
32	704.5	62.7	896	2	US-10-095-929-10	Sequence 10, Appl
33	704.5	62.7	898	1	US-08-693-697-36	Sequence 36, Appl
34	704.5	62.7	906	2	US-08-618-957A-9	Sequence 9, Appli
35	704.5	62.7	906	2	US-09-357-914-32	Sequence 32, Appl
36	704.5	62.7	906	2	US-10-095-929-9	Sequence 9, Appli
37	704.5	62.7	908	1	US-08-693-697-33	Sequence 33, Appl
38	704.5	62.7	923	2	US-08-780-562-4	Sequence 4, Appli
39	704.5	62.7	958	2	US-08-618-957A-8	Sequence 8, Appli
40	704.5	62.7	958	2	US-10-095-929-8	Sequence 8, Appli
41	704.5	62.7	960	1	US-08-355-888A-8	Sequence 8, Appli
42	704.5	62.7	960	1	US-08-693-697-8	Sequence 8, Appli
43	704.5	62.7	960	1	US-08-640-389A-3	Sequence 3, Appli
44	704.5	62.7	960	2	US-08-693-696-8	Sequence 8, Appli
45	704.5	62.7	960	2	US-09-357-914-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-08-803-346-1

; Sequence 1, Application US/08803346

; Patent No. 6281346

; GENERAL INFORMATION:

; APPLICANT: HESS, JOHN W.

; APPLICANT: CASKEY, C. THOMAS

; APPLICANT: LIU, QINGYUN

; APPLICANT: PHILLIPS, MICHAEL SEAN

; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES

; TITLE OF INVENTION: ENCODING THEM

; NUMBER OF SEQUENCES: 77

SCORE Search Results Details for Application 10803459 and Search Result us-10-803-459c-8.rapbm.

Comments /
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OM protein - protein search, using sw model

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Run on:      September 27, 2006, 13:46:06 ; Search time 178 Seconds
              (without alignments)
              543.887 Million cell updates/sec
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Title: US-10-803-459C-8
Perfect score: 1124
Sequence: 1 MAVDVNINIKCETDGYLTKM.....LDGLGYWSNWSRSAYAAVKD 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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3:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description

1	1124	100.0	209	5	US-10-803-459C-8	Sequence 8, Appli
2	713.5	63.5	210	5	US-10-803-459C-2	Sequence 2, Appli
3	709.5	63.1	894	2	US-08-779-457-51	Sequence 51, Appl
4	709.5	63.1	894	4	US-10-079-625-2	Sequence 2, Appli
5	709.5	63.1	894	4	US-10-095-929-12	Sequence 12, Appl
6	709.5	63.1	894	5	US-10-921-710-51	Sequence 51, Appl
7	709.5	63.1	894	6	US-11-026-133-12	Sequence 12, Appl
8	709.5	63.1	894	6	US-11-202-330-2	Sequence 2, Appli
9	709.5	63.1	1162	4	US-10-079-625-43	Sequence 43, Appl
10	709.5	63.1	1162	4	US-10-226-579-2	Sequence 2, Appli
11	709.5	63.1	1162	6	US-11-202-330-43	Sequence 43, Appl
12	704.5	62.7	804	3	US-09-116-676-10	Sequence 10, Appl
13	704.5	62.7	896	2	US-08-779-457-3	Sequence 3, Appli
14	704.5	62.7	896	4	US-10-095-929-10	Sequence 10, Appl
15	704.5	62.7	896	4	US-10-214-802-3	Sequence 3, Appli
16	704.5	62.7	896	4	US-10-373-624A-2	Sequence 2, Appli
17	704.5	62.7	896	5	US-10-774-721-10	Sequence 10, Appl
18	704.5	62.7	896	5	US-10-921-710-3	Sequence 3, Appli
19	704.5	62.7	896	6	US-11-026-133-10	Sequence 10, Appl
20	704.5	62.7	896	6	US-11-192-219-3	Sequence 3, Appli
21	704.5	62.7	906	4	US-10-095-929-9	Sequence 9, Appli
22	704.5	62.7	906	6	US-11-026-133-9	Sequence 9, Appli
23	704.5	62.7	916	4	US-10-373-624A-4	Sequence 4, Appli
24	704.5	62.7	923	2	US-08-779-457-4	Sequence 4, Appli
25	704.5	62.7	923	4	US-10-214-802-4	Sequence 4, Appli
26	704.5	62.7	923	5	US-10-921-710-4	Sequence 4, Appli
27	704.5	62.7	923	6	US-11-192-219-4	Sequence 4, Appli
28	704.5	62.7	925	5	US-10-492-403A-15	Sequence 15, Appl
29	704.5	62.7	958	4	US-10-095-929-8	Sequence 8, Appli
30	704.5	62.7	958	6	US-11-026-133-8	Sequence 8, Appli
31	704.5	62.7	1161	4	US-10-373-624A-8	Sequence 8, Appli
32	704.5	62.7	1161	5	US-10-774-721-14	Sequence 14, Appl
33	704.5	62.7	1165	2	US-08-779-457-2	Sequence 2, Appli
34	704.5	62.7	1165	3	US-09-894-039-1	Sequence 1, Appli
35	704.5	62.7	1165	4	US-10-095-929-11	Sequence 11, Appl
36	704.5	62.7	1165	4	US-10-214-802-2	Sequence 2, Appli
37	704.5	62.7	1165	4	US-10-226-579-4	Sequence 4, Appli
38	704.5	62.7	1165	5	US-10-921-710-2	Sequence 2, Appli
39	704.5	62.7	1165	5	US-10-893-315-73	Sequence 73, Appl
40	704.5	62.7	1165	6	US-11-026-133-11	Sequence 11, Appl
41	704.5	62.7	1165	6	US-11-192-219-2	Sequence 2, Appli
42	704.5	62.7	1165	6	US-11-202-330-4	Sequence 4, Appli
43	704.5	62.7	1167	5	US-10-893-315-87	Sequence 87, Appl
44	704.5	62.7	1234	4	US-10-373-624A-6	Sequence 6, Appli
45	704.5	62.7	1234	5	US-10-774-721-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-803-459C-8

; Sequence 8, Application US/10803459C

; Publication No. US20050209137A1

; GENERAL INFORMATION:

; APPLICANT: Gertler, Arie

; APPLICANT: Krishna, Radha G.

; TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO

; FILE REFERENCE: 28758.1

; CURRENT APPLICATION NUMBER: US/10/803,459C

; CURRENT FILING DATE: 2004-03-19

**SCORE Search Results Details for Application
10803459 and Search Result us-10-803-459c-
8.rapbn.**

Comments /
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GenCore version 5.1.9

```
Run on:      September 27, 2006, 13:47:05 ; Search time 37 Seconds
              (without alignments)
              438.696 Million cell updates/sec
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 285145 seqs, 77663843 residues

Total number of hits satisfying chosen parameters: 285145

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :      Published_Applications_AA_New:*
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2:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	$\frac{\%}{\text{Query}}$
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No.	Score	Match	Length	DB	ID	Description
1	190.5	16.9	422	7	US-11-296-092-32	Sequence 32, Appl
2	190.5	16.9	422	7	US-11-296-155-32	Sequence 32, Appl
3	190.5	16.9	422	7	US-11-300-928-27	Sequence 27, Appl
4	185.5	16.5	918	7	US-11-275-181-6	Sequence 6, Appli
5	160	14.2	836	6	US-10-511-937-2988	Sequence 2988, Ap
6	160	14.2	836	7	US-11-313-104-16	Sequence 16, Appl
7	154	13.7	464	6	US-10-669-920-1407	Sequence 1407, Ap
8	142	12.6	268	6	US-10-669-920-104	Sequence 104, App
9	142	12.6	347	6	US-10-669-920-108	Sequence 108, App
10	142	12.6	374	6	US-10-669-920-102	Sequence 102, App
11	142	12.6	618	6	US-10-669-920-110	Sequence 110, App
12	141.5	12.6	368	6	US-10-449-902-38075	Sequence 38075, A
13	139	12.4	306	6	US-10-669-920-93	Sequence 93, Appl
14	139	12.4	604	6	US-10-669-920-95	Sequence 95, Appl
15	130	11.6	536	6	US-10-669-920-305	Sequence 305, App
16	130	11.6	536	6	US-10-669-920-307	Sequence 307, App
17	129	11.5	538	6	US-10-806-611-6	Sequence 6, Appli
18	123.5	11.0	277	6	US-10-669-920-1405	Sequence 1405, Ap
19	118	10.5	239	7	US-11-353-451-12	Sequence 12, Appl
20	118	10.5	324	7	US-11-353-451-10	Sequence 10, Appl
21	118	10.5	519	7	US-11-301-764-71	Sequence 71, Appl
22	118	10.5	519	7	US-11-353-427-6	Sequence 6, Appli
23	118	10.5	519	7	US-11-353-454-6	Sequence 6, Appli
24	118	10.5	662	7	US-11-301-764-5	Sequence 5, Appli
25	118	10.5	662	7	US-11-353-451-8	Sequence 8, Appli
26	118	10.5	732	7	US-11-353-451-6	Sequence 6, Appli
27	118	10.5	764	7	US-11-301-764-39	Sequence 39, Appl
28	116.5	10.4	819	6	US-10-669-920-523	Sequence 523, App
29	116.5	10.4	825	6	US-10-505-928-650	Sequence 650, App
30	116.5	10.4	825	6	US-10-511-937-3001	Sequence 3001, Ap
31	112.5	10.0	454	6	US-10-669-920-1402	Sequence 1402, Ap
32	110	9.8	501	6	US-10-548-727-6	Sequence 6, Appli
33	110	9.8	635	6	US-10-511-937-2424	Sequence 2424, Ap
34	110	9.8	635	6	US-10-548-727-2	Sequence 2, Appli
35	110	9.8	635	6	US-10-548-727-4	Sequence 4, Appli
36	110	9.8	635	6	US-10-548-727-10	Sequence 10, Appl
37	110	9.8	635	6	US-10-548-727-12	Sequence 12, Appl
38	109	9.7	229	7	US-11-297-134-8	Sequence 8, Appli
39	109	9.7	229	7	US-11-275-181-5	Sequence 5, Appli
40	108	9.6	428	7	US-11-274-375-8	Sequence 8, Appli
41	108	9.6	529	6	US-10-806-611-8	Sequence 8, Appli
42	108	9.6	579	6	US-10-669-920-302	Sequence 302, App
43	108	9.6	629	7	US-11-274-375-10	Sequence 10, Appl
44	102	9.1	335	7	US-11-234-676-321	Sequence 321, App
45	102	9.1	337	7	US-11-274-375-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-11-296-092-32

; Sequence 32, Application US/11296092

; Publication No. US20060105427A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

SCORE Search Results Details for Application 10

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10803459 and Search Result us-10-803-459C-8
[start](#)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 27, 2006, 13:40:15 ; Search time 40 Seconds
(without alignments)
502.733 Million cell updates/sec

Title: US-10-803-459C-8
Perfect score: 1124
Sequence: 1 MAVDVNINIKCETDGYLTKM.....LDGLGYWSNWSRSAYAAVKD 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	712.5	63.4	1162	2 PC4184	leptin receptor, O
2	709.5	63.1	805	2 S68441	leptin receptor, s
3	709.5	63.1	892	2 S68439	leptin receptor, s
4	709.5	63.1	894	2 S68437	leptin receptor, s
5	709.5	63.1	900	2 S68440	leptin receptor, s
6	709.5	63.1	1162	2 S68438	leptin receptor, s
7	700.5	62.3	895	2 S74225	leptin receptor, i
8	185.5	16.5	918	2 A36337	membrane glycoprot

9	175.5	15.6	917	2	I49699	glycoprotein 130 -
10	169	15.0	581	2	I45971	prolactin receptor
11	169	15.0	918	2	A44257	interleukin-6 sign
12	160	14.2	771	2	B38252	granulocyte colony
13	160	14.2	783	2	JH0329	granulocyte colony
14	160	14.2	863	2	C38252	granulocyte colony
15	158.5	14.1	830	2	I50455	prolactin receptor
16	158	14.1	837	2	A34898	granulocyte colony
17	155	13.8	630	2	I51086	prolactin receptor
18	154	13.7	468	1	A41242	interleukin-6 rece
19	149	13.3	831	2	JQ1655	prolactin receptor
20	147	13.1	310	2	A29884	prolactin receptor
21	147	13.1	412	2	A41070	prolactin receptor
22	147	13.1	610	2	A34631	lactogen receptor
23	147	13.1	610	2	A36116	prolactin receptor
24	146.5	13.0	372	2	I58141	ciliary neurotroph
25	144.5	12.9	372	1	UHHUCN	ciliary neurotroph
26	142.5	12.7	362	2	S60614	growth promoting a
27	142	12.6	288	2	B59405	prolactin receptor
28	142	12.6	376	2	A59405	prolactin receptor
29	142	12.6	622	2	A40144	prolactin receptor
30	139	12.4	292	2	I77525	prolactin receptor
31	139	12.4	303	2	I77524	prolactin receptor
32	139	12.4	608	2	I53269	prolactin receptor
33	137.5	12.2	800	1	S31575	interleukin-4 rece
34	135	12.0	616	2	A30304	prolactin receptor
35	118.5	10.5	440	2	JL0144	interleukin-6 rece
36	118.5	10.5	460	2	JL0145	interleukin-6 rece
37	116.5	10.4	825	1	A60386	interleukin-4 rece
38	114	10.1	634	2	S33339	somatotropin recep
39	110	9.8	579	2	B45266	MPL-K protein prec
40	110	9.8	635	2	A45266	MPL-P protein prec
41	109.5	9.7	335	2	A40267	interleukin-5 rece
42	109.5	9.7	625	2	S35317	hematopoietic grow
43	109.5	9.7	626	2	S37622	proto-oncogene - m
44	108.5	9.7	420	2	S21052	interleukin-5 rece
45	108.5	9.7	432	2	I48343	interleukin-11 rec

ALIGNMENTS

RESULT 1

PC4184

leptin receptor, Ob-Rb - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004

C;Accession: JC4895; JC4896; JC4897; PC4184; JC4797

R;Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Tam
Biochem. Biophys. Res. Commun. 225, 75-83, 1996

A;Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identific

A;Reference number: JC4895; MUID:96332408; PMID:8769097

A;Accession: JC4895

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1162

A;Cross-references: UNIPARC:UPI000012E49F; DDBJ:D85558; NID:g1526441; PIDN:BAA12831.1;

A;Accession: JC4896

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-889, 'RADTL'

http://es/ScoreAccessWeb/GetItem.action?AppId=10803459&seqId=669991&ItemName=... 10/3/2006

5	1074	95.6	1147	2	Q9DDK1_MELGA	Q9ddk1 meleagris g
6	731.5	65.1	1166	2	Q4W810_CANFA	Q4w810 canis famil
7	713.5	63.5	1165	1	LEPR_PIG	O02671 sus scrofa
8	712.5	63.4	1162	1	LEPR_RAT	Q62959 rattus norv
9	710.5	63.2	1153	2	Q5XXB8_MYOLU	Q5xxb8 myotis luci
10	709.5	63.1	818	2	Q640Q2_MOUSE	Q640q2 mus musculu
11	709.5	63.1	892	2	Q3UNU8_MOUSE	Q3unu8 mus musculu
12	709.5	63.1	894	2	Q3US58_MOUSE	Q3us58 mus musculu
13	709.5	63.1	1162	1	LEPR_MOUSE	P48356 mus musculu
14	707.5	62.9	890	2	Q5KQU4_BOVIN	Q5kqu4 bos taurus
15	707.5	62.9	895	2	Q59HQ0_BOVIN	Q59hq0 bos taurus
16	707.5	62.9	1165	2	Q5KQU5_BOVIN	Q5kqu5 bos taurus
17	705.5	62.8	895	2	Q863E2_SHEEP	Q863e2 ovis aries
18	704.5	62.7	659	2	Q4G138_HUMAN	Q4g138 homo sapien
19	704.5	62.7	1165	1	LEPR_HUMAN	P48357 homo sapien
20	703.5	62.6	881	2	Q642Z2_MYOLU	Q642z2 myotis luci
21	669.5	59.6	1163	1	LEPR_MACMU	Q9myl0 macaca mula
22	262.5	23.4	884	2	Q6UAM6_TETNG	Q6uam6 tetraodon n
23	209	18.6	918	2	Q9W6U9_CHICK	Q9w6u9 gallus gall
24	190.5	16.9	422	1	CRLF1_HUMAN	O75462 homo sapien
25	187.5	16.7	425	1	CRLF1_MOUSE	Q9jm58 mus musculu
26	186	16.5	567	2	Q4RJ36_TETNG	Q4rj36 tetraodon n
27	185.5	16.5	857	2	Q5FC04_HUMAN	Q5fc04 homo sapien
28	185.5	16.5	918	1	IL6RB_HUMAN	P40189 homo sapien
29	182	16.2	1010	2	Q7TQ89_RAT	Q7tq89 rattus norv
30	175.5	15.6	917	1	IL6RB_MOUSE	Q00560 mus musculu
31	175.5	15.6	917	2	Q6PDI9_MOUSE	Q6pdi9 mus musculu
32	171	15.2	590	2	Q5F4A6_CHICK	Q5f4a6 gallus gall
33	170	15.1	176	2	Q3YA37_XENLA	Q3ya37 xenopus lae
34	169	15.0	581	1	PRLR_BOVIN	Q28172 bos taurus
35	169	15.0	918	1	IL6RB_RAT	P40190 rattus norv
36	167	14.9	581	1	PRLR_CEREL	Q28235 cervus elap
37	166.5	14.8	710	2	O57520_XENLA	O57520 xenopus lae
38	165.5	14.7	389	2	Q6DG28_BRARE	Q6dg28 brachydanio
39	164.5	14.6	819	2	Q6I6F7_EUBMA	Q6i6f7 eublepharis
40	160	14.2	836	1	CSF3R_HUMAN	Q99062 homo sapien
41	158.5	14.1	830	1	PRLR_COLLI	Q90374 columba liv
42	158	14.1	837	1	CSF3R_MOUSE	P40223 mus musculu
43	157.5	14.0	611	2	Q9IBF6_XENLA	Q9ibf6 xenopus lae
44	157.5	14.0	611	2	Q9PTI0_XENLA	Q9pti0 xenopus lae
45	156.5	13.9	394	2	Q6UAQ5_TETNG	Q6uaq5 tetraodon n

ALIGNMENTS

RESULT 1

Q9IBA7_CHICK

ID Q9IBA7_CHICK PRELIMINARY; PRT; 1148 AA.

AC Q9IBA7;

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2000, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE Leptin receptor.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.